

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/526,940  
Source: PG  
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## RAW SEQUENCE LISTING

DATE: 02/27/2006

PATENT APPLICATION: US/10/526,940

TIME: 14:38:35

Input Set : A:\BB-137.ST25.txt

Output Set: N:\CRF4\02272006\J526940.raw

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3 <110> APPLICANT: Deuschle, Ulrich
4      Heck, Stefanie
5      Kober, Ingo
6      Bauer, Ulrike
7      Balogh, Imola
9 <120> TITLE OF INVENTION: NR3B1 Nuclear Receptor Binding 3-Substituted Pyrazoles
11 <130> FILE REFERENCE: BB-137
13 <140> CURRENT APPLICATION NUMBER: 10/526,940
14 <141> CURRENT FILING DATE: 2005-03-08
16 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007066
17 <151> PRIOR FILING DATE: 2003-07-02
19 <150> PRIOR APPLICATION NUMBER: EP 02020256.0
20 <151> PRIOR FILING DATE: 2002-09-10
22 <160> NUMBER OF SEQ ID NOS: 9
24 <170> SOFTWARE: PatentIn version 3.3
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27 <211> LENGTH: 1377
28 <212> TYPE: DNA
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36 acggaacctt ccagcccagc ctccctgacg gacagcgtca accaccacag ccctgggtggc      180
38 tcttcagacg ccagtgggag ctacagttca accatgaatg gccatcagaa cggacttgac      240
40 tcgccacctc tctaccttct tgctcctatc ctgggaggtg gtgggcctgt caggaaactg      300
42 tatgatgact gctccagcac cattgttgaa gatccccaga ccaagtgtga atacatgctc      360
44 aactcgaatg ccaagagact gtgttttagt gtgtgtgaca tcgcttctgg gtaccactat      420
46 ggggtagcat catgtgaagc ctgcaaggca ttcttcaaga ggacaattca aggcaatata      480
48 gaatacagct gccctgccac gaatgaatgt gaaatcacia agcgcagacg taaatcctgc      540
50 caggcttgcc gcttcatgaa gtgttttaaaa gtgggcatgc tgaaagaagg ggtgcgtctt      600
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66 ggccttcttg atctaaataa tgctatcctg cagctggtaa agaaatacaa gagcatgaag      1080
68 ctggaaaaag aagaatttgt caccctcaaa gctatagctc ttgctaattc agactccatg      1140
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72 gattatgaag ctggccagca catggaagac cctcgtcgag ctggcaagat gctgatgaca      1260
74 ctgccactcc tgaggcagac ctctaccaag gccgtgcagc atttctacaa catcaaacta      1320
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87 gatgctcaga aaccacaaag tgcctggtgc ggtgggagga aaaccagagt gtatgctaca      120
89 agcagccggc gggcgccgcc gagtgagggg acgcggcgcg gtggggcggc gcggcccagag      180
91 gaggcggcgg aggagggggc gcccgcggcc cccggctcac tccggcactc cgggcccgtc      240
93 ggcccccatg cctgcccagc cgcgctgccg gagccccagg tgaccagcgc catgtccagc      300
95 caggtggtgg gcattgagcc tctctacatc aaggcagagc cggccagccc tgacagtcca      360
97 aagggttcct cggagacaga gaccgagcct cctgtggccc tggcccctgg tccagctccc      420
99 actcgctgcc tcccaggcca caaggaagag gaggatgggg agggggctgg gcctggcgag      480
101 cagggcggtg ggaagctggt gctcagctcc ctgcccaagc gcctctgcct ggtctgtggg      540
103 gacgtggcct ccggtacca ctatggtgtg gcacctgtg aggcctgcaa agccttcttc      600
105 aagaggacca tccaggggag catcgagtac agctgtccgg cctccaacga gtgtgagatc      660
107 accaagcgga gacgcaaggc ctgccaggcc tgccgcttca ccaagtgcct gcgggtgggc      720
109 atgctcaagg agggagtgcg cctggaccgc gtccggggtg ggcggcagaa gtacaagcgg      780
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125 gaactggggg ctgcctgct gcaactagtg cggcggtgc aggcctgctg gctggagcga      1260
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129 gatgagccga ggctgtggag cagctgcgag aagctcctgc acgaggccct gctggagtat      1380
131 gaagccggcc gggctggccc cggagggggg gctgagcggc ggcgggcggg caggctgctg      1440
133 ctcacgctac cgctcctccg ccagacagcg ggcaaagtgc tggcccattt ctatgggggtg      1500
135 aagctggagg gcaaggtgcc catgcacaag ctgttcttgg agatgtcga ggccatgatg      1566
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141 <211> LENGTH: 25
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145 <400> SEQUENCE: 3
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151 Arg Leu Leu Gln Glu Gly Ser Pro Ser
152          20          25
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156 <211> LENGTH: 29
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 4
161 tcgaggcgat ttgtcaaggt cacacagta      29
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 29

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167 <213> ORGANISM: Homo sapiens
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173 <210> SEQ ID NO: 6
174 <211> LENGTH: 500
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 6
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181 1 5 10 15
184 Lys Thr Glu Pro Ser Ser Pro Ser Ser Gly Ile Asp Ala Leu Ser His
185 20 25 30
188 His Ser Pro Ser Gly Ser Ser Asp Ala Ser Gly Gly Phe Gly Leu Ala
189 35 40 45
192 Leu Gly Thr His Ala Asn Gly Leu Asp Ser Pro Pro Met Phe Ala Gly
193 50 55 60
196 Ala Gly Leu Gly Gly Thr Pro Cys Arg Lys Ser Tyr Glu Asp Cys Ala
197 65 70 75 80
200 Ser Gly Ile Met Glu Asp Ser Ala Ile Lys Cys Glu Tyr Met Leu Asn
201 85 90 95
204 Ala Ile Pro Lys Arg Leu Cys Leu Val Cys Gly Asp Ile Ala Ser Gly
205 100 105 110
208 Tyr His Tyr Gly Val Ala Ser Cys Glu Ala Cys Lys Ala Phe Phe Lys
209 115 120 125
212 Arg Thr Ile Gln Gly Asn Ile Glu Tyr Ser Cys Pro Ala Thr Asn Glu
213 130 135 140
216 Cys Glu Ile Thr Lys Arg Arg Arg Lys Ser Cys Gln Ala Cys Arg Phe
217 145 150 155 160
220 Met Lys Cys Leu Lys Val Gly Met Leu Lys Glu Gly Val Arg Leu Asp
221 165 170 175
224 Arg Val Arg Gly Gly Arg Gln Lys Tyr Lys Arg Arg Leu Asp Ser Glu
225 180 185 190
228 Ser Ser Pro Tyr Leu Ser Leu Gln Ile Ser Pro Pro Ala Lys Lys Pro
229 195 200 205
232 Leu Thr Lys Ile Val Ser Tyr Leu Leu Val Ala Glu Pro Asp Lys Leu
233 210 215 220
236 Tyr Ala Met Pro Pro Pro Gly Met Pro Glu Gly Asp Ile Lys Ala Leu
237 225 230 235 240
240 Thr Thr Leu Cys Asp Leu Ala Asp Arg Glu Leu Val Val Ile Ile Gly
241 245 250 255
244 Trp Ala Lys His Ile Pro Gly Phe Ser Ser Leu Ser Leu Gly Asp Gln
245 260 265 270
248 Met Ser Leu Leu Gln Ser Ala Trp Met Glu Ile Leu Ile Leu Gly Ile
249 275 280 285
252 Val Tyr Arg Ser Leu Pro Tyr Asp Asp Lys Leu Val Tyr Ala Glu Asp
253 290 295 300
256 Tyr Ile Met Asp Glu Glu His Ser Arg Leu Ala Gly Leu Leu Glu Leu
257 305 310 315 320

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260 Tyr Arg Ala Ile Leu Gln Leu Val Arg Arg Tyr Lys Lys Leu Lys Val  
 261 325 330 335  
 264 Glu Lys Glu Glu Phe Val Thr Leu Lys Ala Leu Ala Leu Ala Asn Ser  
 265 340 345 350  
 268 Asp Ser Met Tyr Ile Glu Asp Leu Glu Ala Val Gln Lys Leu Gln Asp  
 269 355 360 365  
 272 Leu Leu His Glu Ala Leu Gln Asp Tyr Glu Leu Ser Gln Arg His Glu  
 273 370 375 380  
 276 Glu Pro Trp Arg Thr Gly Lys Leu Leu Leu Thr Leu Pro Leu Leu Arg  
 277 385 390 395 400  
 280 Gln Thr Ala Ala Lys Ala Val Gln His Phe Tyr Ser Val Lys Leu Gln  
 281 405 410 415  
 284 Gly Lys Val Pro Met His Lys Leu Phe Leu Glu Met Leu Glu Ala Lys  
 285 420 425 430  
 288 Ala Trp Ala Arg Ala Asp Ser Leu Gln Glu Trp Arg Pro Leu Glu Gln  
 289 435 440 445  
 292 Val Pro Ser Pro Leu His Arg Ala Thr Lys Arg Gln His Val His Phe  
 293 450 455 460  
 296 Leu Thr Pro Leu Pro Pro Pro Pro Ser Val Ala Trp Val Gly Thr Ala  
 297 465 470 475 480  
 300 Gln Ala Gly Tyr His Leu Glu Val Phe Leu Pro Gln Arg Ala Gly Trp  
 301 485 490 495  
 304 Pro Arg Ala Ala  
 305 500

308 &lt;210&gt; SEQ ID NO: 7

309 &lt;211&gt; LENGTH: 1503

310 &lt;212&gt; TYPE: DNA

311 &lt;213&gt; ORGANISM: Homo sapiens

313 &lt;400&gt; SEQUENCE: 7

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 316 tccagcccg cctcgggcat agatgccctc agccaccaca gcccagtggt ctggtccgac 120  
 318 gccagcggcg gctttggcct ggccctgggc acccagccca acggtctgga ctgcacccc 180  
 320 atgtttgcag gcgcccggct gggaggcacc ccatgccgca agagctacga ggactgtgcc 240  
 322 agcggcatca tggaggactc ggccatcaag tgcgagtaca tgctcaacgc catccccaag 300  
 324 cgctgtgtcc tcgtgtgcgg ggacattgcc tctggctacc actacggcgt ggcctcctgc 360  
 326 gaggttgca aggccttctt caagaggact atccaaggga acattgagta cagctgcccg 420  
 328 gccaccaacg agtgcgagat caccaaacgg aggcgcaagt cctgccaggc ctgccgcttc 480  
 330 atgaaatgcc tcaaagtggg gatgctgaag gaaggtgtgc gccttgatcg agtgcgtgga 540  
 332 ggccgtcaga aatacaagcg acggctggac tcagagagca gccatacct gagcttacia 600  
 334 atttctccac ctgctaaaaa gccattgacc aagattgtct catacctact ggtggctgag 660  
 336 ccggacaagc tctatgccat gcctccccct ggtatgcctg agggggacat caaggccctg 720  
 338 accactctct gtgacctggc agaccgagag cttgtggtca tcattggctg ggccaagcac 780  
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 342 atggaaatcc tcatcctggg catcgtgtac cgctcgctgc cctacgacga caagctgggtg 900  
 344 tacgctgagg actacatcat ggatgaggag cactcccgcc tcgcggggct gctggagctc 960  
 346 taccgggcca tcctgcagct ggtacgcagg tacaagaagc tcaagtgga gaaggaggag 1020  
 348 tttgtgacgc tcaaggccct ggccctcgcc aactccgatt ccatgtacat cgaggatcta 1080  
 350 gaggtgtcc agaagctgca ggacctgtg cagcaggcac tgcaggacta cgagctgagc 1140  
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356 atgcacaaac tcttcctgga gatgctggag gccaaggcct gggccagggc tgactccctt 1320
358 caggagtgga ggccactgga gcaagtgtcc tctcccctcc accgagccac caagaggcag 1380
360 catgtgcatt tcctaactcc cttgccccct ccccatctg tggcctgggt gggcactgct 1440
362 caggctggat accacctgga ggttttcctt ccgcagaggg caggttggtc aagagcagct 1500
364 tag 1503
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368 <211> LENGTH: 436
369 <212> TYPE: PRT
370 <213> ORGANISM: Homo sapiens
372 <400> SEQUENCE: 8
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378 Lys Thr Glu Pro Ser Ser Pro Ala Ser Leu Thr Asp Ser Val Asn His
379 20 25 30
382 His Ser Pro Gly Gly Ser Ser Asp Ala Ser Gly Ser Tyr Ser Ser Thr
383 35 40 45
386 Met Asn Gly His Gln Asn Gly Leu Asp Ser Pro Pro Leu Tyr Pro Ser
387 50 55 60
390 Ala Pro Ile Leu Gly Gly Ser Gly Pro Val Arg Lys Leu Tyr Asp Asp
391 65 70 75 80
394 Cys Ser Ser Thr Ile Val Glu Asp Pro Gln Thr Lys Cys Glu Tyr Met
395 85 90 95
398 Leu Asn Ser Met Pro Lys Arg Leu Cys Leu Val Cys Gly Asp Ile Ala
399 100 105 110
402 Ser Gly Tyr His Tyr Gly Val Ala Ser Cys Glu Ala Cys Lys Ala Ser
403 115 120 125
406 Phe Lys Arg Lys Ile Gln Ala Asn Ile Glu Tyr Ser Cys Pro Ala Thr
407 130 135 140
410 Asn Glu Cys Glu Ile Thr Lys Arg Arg Arg Lys Ser Cys Gln Ala Cys
411 145 150 155 160
414 Arg Phe Met Lys Cys Leu Lys Val Gly Met Leu Lys Glu Gly Val Arg
415 165 170 175
418 Leu Asp Arg Val Arg Gly Gly Arg Gln Lys Tyr Lys Arg Arg Ile Asp
419 180 185 190
422 Ala Glu Asn Ser Pro Tyr Leu Asn Pro Gln Leu Val Gln Pro Ala Lys
423 195 200 205
426 Lys Pro Tyr Asn Lys Ile Val Ser His Leu Leu Val Ala Glu Pro Glu
427 210 215 220
430 Lys Ile Tyr Ala Met Pro Asp Pro Thr Val Pro Asp Ser Asp Ile Lys
431 225 230 235 240
434 Ala Leu Thr Thr Leu Cys Asp Cys Ala Asp Arg Glu Leu Val Val Ile
435 245 250 255
438 Ile Gly Trp Ala Lys His Ile Pro Gly Phe Ser Thr Leu Ser Leu Ala
439 260 265 270
442 Asp Gln Met Ser Leu Leu Gln Ser Ala Trp Met Glu Ile Leu Ile Leu
443 275 280 285
446 Gly Phe Val Tyr Arg Ser Leu Ser Phe Glu Asp Glu Leu Val Tyr Ala
447 290 295 300

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**VERIFICATION SUMMARY**

DATE: 02/27/2006

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